

SEQUENCE LISTING

<110> Xia, Zhi-Qiang
 Costa, Michael A
 Davin, Laurence B
 Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and
 methods of Use

<130> wsurl13787

<140> Not yet assigned
 <141> 1999-04-23

<150> 60/082,977
 <151> 1998-04-24

<160> 25

<170> PatentIn Ver. 2.0

<210> 1
 <211> 819
 <212> DNA
 <213> Forsythia x intermedia

<220>
 <221> CDS
 <222> (1)..(819)

<400> 1	48
atg cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc	
Met Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala	
1 5 10 15	
ctt ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc	96
Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu	
20 25 30	
ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa	144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu	
35 40 45	
tta ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac	192
Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr	
50 55 60	
atc cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac	240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp	
65 70 75 80	
aac aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca	288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala	
85 90 95	
gga att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca	336
Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala	
100 105 110	

100	105	110	
gac ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys 115	120	125	384
atg aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile 130	135	140	432
att tcc act gct agt tta agc tca act atg ggt ggt tct tca cat Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His 145	150	155	480
gcc tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu 165	170	175	528
gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro 180	185	190	576
ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat Phe Gly Leu Pro Thr Ala Leu Gly Lys Phe Ser Gly Ile Lys Asn 195	200	205	624
gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly 210	215	220	672
cca aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Leu Tyr Leu Ala 225	230	235	720
agt gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly 245	250	255	768
ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp 260	265	270	816
tct Ser			819
<210> 2			
<211> 273			
<212> PRT			
<213> <i>Forsythia x intermedia</i>			
<400> 2			
Met Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala 1 5 10 15			
Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu 20 25 30			

Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
 35 40 45

Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr
 50 55 60

Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65 70 75 80

Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala
 85 90 95

Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala
 100 105 110

Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys
 115 120 125

Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile
 130 135 140

Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His
 145 150 155 160

Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu
 165 170 175

Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
 180 185 190

Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn
 195 200 205

Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly
 210 215 220

Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala
 225 230 235 240

Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly
 245 250 255

Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp
 260 265 270

Ser

<210> 3
 <211> 831
 <212> DNA
 <213> Forsythia x intermedia

<220>
 <221> CDS
 <222> (1)..(831)

<400> 3
atg gca gcc act tca cag gtt cta act gca atc gca aga agg cta gaa 48
Met Ala Ala Thr Ser Gln Val Leu Thr Ala Ile Ala Arg Arg Leu Glu
1 5 10 15

gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa acc 96
Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr
20 25 30

aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat 144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
35 40 45

gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc act tcc 192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
50 55 60

aat tcc acc tac atc cac tgt gat gtt act aat gaa gac ggt gtt aaa 240
Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys
65 70 75 80

aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg 288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met
85 90 95

ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac 336
Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp
100 105 110

aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga 384
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly
115 120 125

gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc 432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg
130 135 140

agt ggc aac ata att tcc act gct agt tta agc tca act atg ggt ggt 480
Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly
145 150 155 160

ggt tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt 528
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu
165 170 175

act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat 576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn
180 185 190

tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca 624
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
195 200 205

ggg att aaa aat gaa gaa ttt gag aat gta ata aac ttt gcg gga 672
Gly Ile Lys Asn Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
210 215 220

aat ctg aaa ggt cca aaa ttt aat gtt gag gat gtt gcc aat gca gct 720

Asn	Leu	Lys	Gly	Pro	Lys	Phe	Asn	Val	Glu	Asp	Val	Ala	Asn	Ala	Ala
225					230				235						240
ctt	tat	ctg	gct	agt	gat	gag	gca	aaa	tac	gtg	agt	gga	cac	aat	ctg
Leu	Tyr	Leu	Ala	Ser	Asp	Glu	Ala	Lys	Tyr	Val	Ser	Gly	His	Asn	Leu
															245
															250
															255
ttc	att	gat	gga	ggg	ttc	agc	gtc	tgc	aat	tct	gta	atc	aaa	gtg	ttc
Phe	Ile	Asp	Gly	Gly	Phe	Ser	Val	Cys	Asn	Ser	Val	Ile	Lys	Val	Phe
															260
															265
															270
caa	tat	cca	gat	tct											831
Gln	Tyr	Pro	Asp	Ser											
															275
<210> 4															
<211> 277															
<212> PRT															
<213> Forsythia x intermedia															
<400> 4															
Met	Ala	Ala	Thr	Ser	Gln	Val	Leu	Thr	Ala	Ile	Ala	Arg	Arg	Leu	Glu
1					5						10				15
Gly	Lys	Val	Ala	Leu	Ile	Thr	Gly	Gly	Ala	Ser	Gly	Ile	Gly	Glu	Thr
					20					25					30
Thr	Ala	Lys	Leu	Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp
										35		40			45
Val	Gln	Asp	Glu	Leu	Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser
										50		55			60
Asn	Ser	Thr	Tyr	Ile	His	Cys	Asp	Val	Thr	Asn	Glu	Asp	Gly	Val	Lys
										65		70			80
Asn	Ala	Val	Asp	Asn	Thr	Val	Ser	Thr	Tyr	Gly	Lys	Leu	Asp	Ile	Met
										85		90			95
Phe	Ser	Asn	Ala	Gly	Ile	Ser	Asp	Pro	Asn	Arg	Pro	Arg	Ile	Ile	Asp
										100		105			110
Asn	Glu	Lys	Ala	Asp	Phe	Glu	Arg	Val	Phe	Ser	Val	Asn	Val	Thr	Gly
												115		120	125
Val	Phe	Leu	Cys	Met	Lys	His	Ala	Ala	Arg	Val	Met	Ile	Pro	Ala	Arg
											130		135		140
Ser	Gly	Asn	Ile	Ile	Ser	Thr	Ala	Ser	Leu	Ser	Ser	Thr	Met	Gly	Gly
												145		150	155
Gly	Ser	Ser	His	Ala	Tyr	Cys	Gly	Ser	Lys	His	Ala	Val	Leu	Gly	Leu
											165		170		175
Thr	Arg	Asn	Leu	Ala	Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn
										180		185			190

Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser
 195 200 205
 Gly Ile Lys Asn Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly
 210 215 220
 Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala
 225 230 235 240
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
 245 250 255
 Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe
 260 265 270
 Gln Tyr Pro Asp Ser
 275

<210> 5
 <211> 819
 <212> DNA
 <213> Forsythia x intermedia

<220>
 <221> CDS
 <222> (1)..(819)

<400> 5
 atg cag ctt cga act gca atc gca aga agg cta gaa gga aaa gtt gcc 48
 Met Gln Leu Arg Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala
 1 5 10 15
 ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca gca aaa ctc 96
 Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu
 20 25 30
 ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144
 Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu
 35 40 45
 tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac 192
 Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
 50 55 60
 atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65 70 75 80
 aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca 288
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala
 85 90 95
 gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca 336
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
 100 105 110
 gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt 384

Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe			
115	120	125	
atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata		432	
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile			
130	135	140	
att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat		480	
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His			
145	150	155	160
gct tat tgt gca aaa cat gct gta tta ggc ctt act agg aat ctg		528	
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu			
165	170	175	
gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct		576	
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro			
180	185	190	
ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat		624	
Phe Gly Leu Pro Thr Pro Leu Ala Lys Phe Ser Gly Ile Glu Asn			
195	200	205	
gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt		672	
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly			
210	215	220	
aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt ttt ctg gct		720	
Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala			
225	230	235	240
agt gat gag gca caa tat gtg agt gga caa aat ctg ttc atc gat gga		768	
Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly			
245	250	255	
ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac		816	
Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp			
260	265	270	
tct		819	
Ser			

<210> 6

<211> 273

<212> PRT

<213> Forsythia x intermedia

<400> 6

Met Gln Leu Arg Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala

1

5

10

15

Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu

20

25

30

Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu

35

40

45

Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
 50 55 60
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65 70 75 80
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala
 85 90 95
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
 100 105 110
 Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe
 115 120 125
 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile
 130 135 140
 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His
 145 150 155 160
 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu
 165 170 175
 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
 180 185 190
 Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
 195 200 205
 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
 210 215 220
 Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
 225 230 235 240
 Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly
 245 250 255
 Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
 260 265 270

Ser

<210> 7
 <211> 831
 <212> DNA
 <213> *Forsythia x intermedia*

<220>
 <221> CDS
 <222> (1)..(831)

<400> 7
 atg gcc agt act tca cag gtt cta act gca atc aca aga agg cta gaa 48
 Met Ala Ser Thr Ser Gln Val Leu Thr Ala Ile Thr Arg Arg Leu Glu

1	5	10	15	
gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa ttc Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe	20	25	30	96
aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp	35	40	45	144
gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc atc ggc act tcc Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser	50	55	60	192
aat tcc atc tac atc cac tgc gat gtt acc aat gaa gac gat gtt aaa Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys	65	70	75	240
aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met	85	90	95	288
ttc aac aat gca gga att gct gac ccc aac aag ccc cgc atc gta gac Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp	100	105	110	336
aac gaa aaa gca gac ttt gaa cgc gtt ctc agc gta aat gta acc ggt Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly	115	120	125	384
gtt ttc cta tgc atg aag cac gca gca cgc gtt atg gtg cca gca cgc Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg	130	135	140	432
agt ggc agc ata att tcc act gct agc gta agc tca aca att ggt ggt Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly	145	150	155	480
gct gct tca cat gct tat tgt tca aag cat gct gtg tta ggc ctt Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu	165	170	175	528
act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn	180	185	190	576
tgt ttg gct cct tac gcg ctt gct acg cct tta gcc aag aaa ttt gta Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val	195	200	205	624
ggg ctt gaa aat gac gaa gat ttg gag aat gca atg agc ctt atg gga Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly	210	215	220	672
aat ctg aaa ggt aca aat ttg aag gct gag gac gtc gcc aat gca gct Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala	225	230	235	720

-10-

ctt tat ctg gca agt gat gag gca aaa tat gtg agt gga cac aat ctg	768		
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu			
245	255		
ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc	816		
Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe			
260	265	270	
caa tat cca gac act	831		
Gln Tyr Pro Asp Thr			
275			
<210> 8			
<211> 277			
<212> PRT			
<213> Forsythia x intermedia			
<400> 8			
Met Ala Ser Thr Ser Gln Val Leu Thr Ala Ile Thr Arg Arg Leu Glu			
1	5	10	15
Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe			
20	25	30	
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp			
35	40	45	
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser			
50	55	60	
Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys			
65	70	75	80
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met			
85	90	95	
Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp			
100	105	110	
Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly			
115	120	125	
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg			
130	135	140	
Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly			
145	150	155	160
Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu			
165	170	175	
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn			
180	185	190	
Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val			
195	200	205	

Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly
 210 215 220
 Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala
 225 230 235 240
 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu
 245 250 255
 Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Ala Ile Lys Met Phe
 260 265 270
 Gln Tyr Pro Asp Thr
 275

<210> 9
 <211> 828
 <212> DNA
 <213> Forsythia x intermedia

<220>
 <221> CDS
 <222> (1)..(828)

<400> 9
 atg gcc act tca cag ctt cga act gca ttc gca aga agg cta gaa gga 48
 Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
 1 5 10 15
 aaa gtt gcc ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca 96
 Lys Val Ala Leu Ile Thr Gly Ala Ser Gly Val Gly Glu Val Thr
 20 25 30
 gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc 144
 Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
 35 40 45
 caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat 192
 Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
 50 55 60
 tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat 240
 Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65 70 75 80
 gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc 288
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
 85 90 95
 aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac 336
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
 100 105 110
 gaa aaa gca gac ttt gaa cgc gtt ctc agt gtt aat gta acc gga gtt 384
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
 115 120 125

ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt	432
Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser	
130	135
140	
ggc tgc ata att tcc act gct agt tta agc tca act atg ggt ggt ggt	480
Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly	
145	150
155	160
tct tca cat gct tat tgt ggt tca aag cat gct gta tta ggc ctt act	528
Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr	
165	170
175	
agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt	576
Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys	
180	185
190	
ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg	624
Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Phe Thr Gly	
195	200
205	
att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat	672
Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn	
210	215
220	
ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt	720
Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu	
225	230
235	240
ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc	768
Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe	
245	250
255	
atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa	816
Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln	
260	265
270	
tat cca gac tct	828
Tyr Pro Asp Ser	
275	

<210> 10

<211> 276

<212> PRT

<213> *Forsythia x intermedia*

<400> 10

Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly

1

5

10

15

Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr

20

25

30

Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val

35

40

45

Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn

50

55

60

Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65 70 75 80
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
 85 90 95
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
 100 105 110
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
 115 120 125
 Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
 130 135 140
 Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
 145 150 155 160
 Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
 165 170 175
 Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
 180 185 190
 Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
 195 200 205
 Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
 210 215 220
 Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu
 225 230 235 240
 Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe
 245 250 255
 Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln
 260 265 270
 Tyr Pro Asp Ser
 275

<210> 11
 <211> 21
 <212> PRT
 <213> *Forsythia x intermedia*

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> N-terminal peptide of *F. intermedia*
 secoisolariciresinol protein wherein Xaa at
 positions 3, 12 and 20 represents an unidentified
 amino acid residue

<400> 11

-14-

Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu
1 5 10 15

Ile Thr Gly Xaa Ala
20

<210> 12

<211> 17

<212> PRT

<213> Forsythia x intermedia

<400> 12

Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala
1 5 10 15

Lys

<210> 13

<211> 15

<212> PRT

<213> Forsythia x intermedia

<400> 13

Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys
1 5 10 15

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> PCR primer wherein n at positions 3, 9, 15 and 18
represents inosine

<400> 14

ggnathggng aracnacngc

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 15
ccngcrttng arAACATDAT

20

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 16
ccngcrttnc traACATDAT

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer

<400> 17
attccgcttag attgcattga

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature

<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represent inosine

<400> 18
ccngcrttnc traacatdat

20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> T7 PCR primer

<400> 19
aattaaacct cactaaaggg

20

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer

<400> 20
cagttcgaa ctgcattcgc aag

23

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(22)
<223> T7 PCR primer

<400> 21	22
cgggatatca ctcagcataa tg	
<210> 22	
<211> 816	
<212> DNA	
<213> <i>Forsythia x intermedia</i>	
<220>	
<221> CDS	
<222> (1)..(816)	
<400> 22	48
cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt	
Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu	
1 5 10 15	
ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc	96
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe	
20 25 30	
tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta	144
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu	
35 40 45	
ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc	192
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile	
50 55 60	
cac tgt gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac aac	240
His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn	
65 70 75 80	
aca gtt tca acc tat gga aaa ctg gac att atg ttc agc aat gca gga	288
Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly	
85 90 95	
att tct gat ccc aac agg ccc cgc atc ata gac aac gaa aaa gca gac	336
Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp	
100 105 110	
ttt gaa cgc gtt ctc agt gta aat gta acc gga gtt ttc cta tgc atg	384
Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met	
115 120 125	
aag cac gca gca cgt gtt atg att cca gca cgc agt ggc aac ata att	432
Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile	
130 135 140	
tcc act gct agt tta agc tca act atg ggt ggt tct tca cat gcc	480
Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His Ala	
145 150 155 160	
tat tgt ggt tca aag cat gct gtg tta gcc ctt act agg aat ctg gca	528
Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala	
165 170 175	

-18-

gtc gag ctc gga caa ttt ggc att agg gtt aat tgt ttg tct cct ttc	576
Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe	
180 185 190	
ggg ctt cct acg gct tta ggc aag aaa ttt tca ggg att aaa aat gaa	624
Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu	
195 200 205	
gaa gaa ttt gag aat gta ata aac ttt gcg gga aat ttg aaa ggt cca	672
Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro	
210 215 220	
aaa ttt aat gtt gag gat gtt gcc aat gca gct ctt tat ctg gct agt	720
Lys Phe Asn Val Glu Asp Val Ala Asn Ala Leu Tyr Leu Ala Ser	
225 230 235 240	
gat gag gca aaa tac gtg agt gga cac aat ctg ttc att gat gga ggg	768
Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly	
245 250 255	
ttc agc gtc tgc aat tct gta atc aaa gtg ttc caa tat cca gat tct	816
Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser	
260 265 270	

<210> 23

<211> 272

<212> PRT

<213> *Forsythia x intermedia*

<400> 23

Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu	
1 5 10 15	

Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe	
20 25 30	

Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu	
35 40 45	

Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile	
50 55 60	

His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn	
65 70 75 80	

Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly	
85 90 95	

Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp	
100 105 110	

Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met	
115 120 125	

Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile	
130 135 140	

-19-

Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala
145 150 155 160

Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala
165 170 175

Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe
180 185 190

Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu
195 200 205

Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro
210 215 220

Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser
225 230 235 240

Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly
245 250 255

Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser
260 265 270

<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
<223> PCR primer

<400> 24
acatatgcag cttcgaaactg cattcgcaag aag

33

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
<223> PCR primer

<400> 25

0967348 010201

WO 99/55846

PCT/US99/08975

-20-

catatggca gacatgttac atgatcaatt gca

33